

Figure S3. Composite of mapped reads across all samples for exon 1ext. The depth of mapped reads is indicated by the gray histogram in the upper panel, while HTR2A gene structure is depicted in the lower panel (3'-to-5' direction from left-to-right). The histogram suggests the presence of at least two different transcription start sites (arrows), which coincide with predicted sites from Eponine (Down & Hubbard, 2002). Note: read depth is presented in linear scale.